




PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Bio

Search for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: [U95825](#)[gi:4539617] This record was replaced or removed. See [revision history](#) for details.

LOCUS HSU95825 4392 bp mRNA linear PRI 30-MAR-1999
 DEFINITION Human androgen-induced prostate proliferative shutoff associated
 protein (AS3) mRNA, complete cds.
 ACCESSION U95825
 VERSION U95825.1 GI:4539617
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Soto,A.M. and Sonnenschein,C.
 TITLE Androgen-induced proliferative shutoff in prostate cancer cells
 JOURNAL Proc. Annu. Meet. Am. Assoc. Cancer Res. 37, 223-223 (1996)
 REFERENCE 2 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Sonnenschein,C. and Soto,A.M.
 TITLE Early gene expression during androgen-induced inhibition of
 proliferation of prostate cancer cells: a new suppressor candidate
 on chromosome 13, in the BRCA2-Rb1 locus
 JOURNAL J. Steroid Biochem. Mol. Biol. 68, 41-45 (1999)
 REFERENCE 3 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Sonnenschein,C. and Soto,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Anatomy and Cell Biology, Tufts University
 Medical School, 136 Harrison Avenue, Boston, MA 02111, USA
 COMMENT [WARNING] On Apr 5, 1999 this sequence was replaced by a newer
 version [gi:4559409](#).
 FEATURES
 source Location/Qualifiers
 1..4392
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="13"
 /map="13q12-q13"
 /cell_line="LNCaP"
 /cell_type="cancer cells"
 /tissue_type="prostate"
 /note="exons 1-21 map to cosmid 267p19; exons 22-31 map to
 cosmid PAC49J10"
 gene 1..4392
 /gene="AS3"
 exon 1..46
 /gene="AS3"
 /number=1
 exon 47..144
 /gene="AS3"
 /number=2
 exon 145..271

CDS /gene="AS3"
/number=3
170..3823
/gene="AS3"
/codon_start=1
/product="androgen-induced prostate proliferative shutoff
associated protein"
/protein_id="AAD22134.1"
/db_xref="GI:4539618"
/translation="MHMVDLMSSIIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLA
KALLKRTAQAIEPYITTFNQLMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQ
LEFKLKSNDNEERLQVVKLLAKMFGAKDSELASQNKPLWQCYLGRFNDIHVPIRLECV
KFASHCLMNHPDLAKDLTEYLLKVRSHDPEEAIRHDTVIVSIVTAAKKDILLVNDHLLNF
VRERTLDKRWRVRKEAMMGLAQIYKKYALQSAAGKDAKQIAWIKDKLLHIYYQNSID
DRLLVERIFAQYMPHNLETTERMKCLYYLYATLDLNAVKALNEMWKCQNLLRHQVKD
LLDLIKQPKTDASVKAI FSKVMVITRNLDPGKAQDFMKKFTQVLEDEKIRKQLEVL
VSPTCSCKQAEGCVREITTKLGNPKQPTNPFLEMIKFLLEIAPVHIDTESISALIKQ
VNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTHPISFHS AETFESLLACLKMDDE
KVAAEALQIFKNTGSKI EEDFPHIRSALLPVLHHKSKKGPPRQAKYAIHCHAI FSSK
ETQFAQIF EPLHKS LDPSNLEHLITPLVTIGHIAL LAPDQFAAPWKS WATF FIVKDLL
MNDRLPGKKT TTKLWVPDEEVSPETMVKIQA IKMMVRWLLGMKNNHSGTSTLRLTT
ILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEP CYHEIITLEQYQLCALAINDE
CYQVRQVFAQKLHKGLSRLRPLEYMAICALCAKDPVKERRAHARQCLVKINVRREY
LKQHA AVSEKLLSLLPEYVVPYTIHLLAHD PDYVKVQDIEQLKDVKECLWFVLEILMA
KNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVCDVAMNIIMSKSTTYSLESP
KDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTTNVLGAVNKPLSSAGKQSQ
TKSSRMETVSNASSSSNPSSPGRIKGRLDSSSEMDHSENE DYTMS SPLPGKKS DKRDDS
DLVRSELEKPRGRKKT PVTEQEEKLGMDDLTKLVQE QKPKGSQSRKRGTASESDEQ
QWPEEKRLKEDI LENEDEQNSPPKKGKGRPPKPLGGGTPKEEPTMKTSKKGSKKKSG
PPAPEEEEEERQSGNTEQKSKSKQHRVSRRAQQAESPESSAIESTQSTPQKGRGRP
SKTPSPSQPKKNV"
exon 272..352
/gene="AS3"
/number=4
exon 353..493
/gene="AS3"
/number=5
exon 494..609
/gene="AS3"
/number=6
exon 610..704
/gene="AS3"
/number=7
exon 705..850
/gene="AS3"
/number=8
exon 851..1002
/gene="AS3"
/number=9
exon 1003..1116
/gene="AS3"
/number=10
exon 1117..1198
/gene="AS3"
/number=11
exon 1199..1247
/gene="AS3"
/number=12
exon 1248..1387
/gene="AS3"

exon /number=13
1388..1503
/gene="AS3"
/number=14
exon 1504..1609
/gene="AS3"
/number=15
exon 1610..1770
/gene="AS3"
/number=16
exon 1771..1894
/gene="AS3"
/number=17
exon 1895..2053
/gene="AS3"
/number=18
exon 2054..2122
/gene="AS3"
/number=19
exon 2123..2259
/gene="AS3"
/number=20
exon 2260..2383
/gene="AS3"
/number=21
exon 2384..2588
/gene="AS3"
/number=22
exon 2589..2703
/gene="AS3"
/number=23
exon 2704..2836
/gene="AS3"
/number=24
exon 2837..2956
/gene="AS3"
/number=25
exon 2957..3019
/gene="AS3"
/number=26
exon 3020..3165
/gene="AS3"
/number=27
exon 3166..3271
/gene="AS3"
/number=28
exon 3272..3711
/gene="AS3"
/number=29
exon 3712..3936
/gene="AS3"
/number=30
exon 3937..4392
/gene="AS3"
/number=31

BASE COUNT 1508 a 801 c 894 g 1189 t
ORIGIN

1 ggatacaaag agcccacaat tcaataggta tttttattta cttgagaaca ttgcttgggt
61 caagtcatat aacatatgct ttgagttaga agatagcaat gaaattttca cccagctata
121 cagaacctta ttttcagtta taaacaatgg ccacaatcag aaagtccata tgcacatggt

```
181 agaccttatg agctctatta tttgtgaagg tgatacagtg tctcaggagc ttttggatac
241 ggttttagta aatctggtac ctgctcataa gaatttaaac aagcaagcat atgatttggc
301 aaaggcttta ctgaagagga cagctcaagc tattgagcca tatattacca ctttttttaa
361 tcaggttctg atgcttggga aaacatctat cagcgatttg tcagagcatg tctttgactt
421 aattttggag ctctacaata ttgatagtca tttgctgctc tctgttttac cccagcttga
481 attttaaatta aagagcaatg ataatgagga ggcctacaa gttgttaaac tactggcaaa
541 aatgtttggg gcaaaggatt cagaattggc ttctcaaaac aagccacttt ggcagtgtca
601 cttgggcagg tttaatgata tccatgtacc aatccgcctg gaatgtgtga aatttgctag
661 ccattgtctc atgaaccatc ctgatttagc aaaagactta acagagtatic ttaaagttag
721 gtcacatgac cctgaggaag ctattagaca tgatgttatt gtgtcaatag ttacagctgc
781 taaaaaggat attcttctgg tcaatgatca cttacttaat tttgtgagag agagaacatt
841 agacaaacga tggagagtac gcaaagaagc catgatggga cttgccccaa tttataagaa
901 atatgcttta cagtcagcag ctggaaaaga tgctgcaaaa cagatagcat ggatcaaaga
961 caaattgcta catatatatt atcaaaatag tattgatgat cgactacttg ttgaacggat
1021 ctttgctcaa tacatgggtc ctcacaattt agaaactaca gaacggatga aatgcttata
1081 ttacttgtat gccacactgg attttaaagc tgtgaaagca ttgaatgaaa tgtggaaatg
1141 tcaaaatctg ctccgacatc aagtaaagga tttgcttgac ttgattaagc aacccaaaac
1201 agatgccagt gtcaaggcca tattttcaaa agtgatggtt attacaagaa atttacctga
1261 tcctggtaag gctcaggatt tcatgaagaa attcacacag gtgttagaag atgatgagaa
1321 aataagaaag cagttagaag tacttgttag tccaacatgc tcctgaagc aggctgaagg
1381 ttgtgtgcgt gaaataacta agaagtggg caaccccaaa cagcctacaa atcctttcct
1441 ggaaatgatc aagtttctct tggagaggat agcacctgtg cacatagata ccgaatctat
1501 cagtgtctct attaaacaag tgaacaaatc aatagatgga acagcagatg atgaagtga
1561 ggggtgtcca actgatcaag ccatcagagc aggtcttgaa ctgcttaagg tactctcatt
1621 tacacatccc atctcatttc attctgctga aacatttgaa tcattactgg cttgtctgaa
1681 aatggatgat gaaaaagtag cagaagctgc actacaaatt ttcaaaaaca caggaagcaa
1741 aattgaagag gattttccac acatcagatc agccttgctt cctgttttac atcacaaatc
1801 taaaaaagga ccccccgtc aagccaaata tgccattcat tgtatccatg cgatattttc
1861 tagtaaagag acccagtttg cagagatatt tgagcctctg cataagagcc tagatccaag
1921 caacctggaa catctcataa caccattggt tactattggt catattgctc tccttgacc
1981 tgatcaattt gctgtcctt ggaaatcttg ggtagctact ttcattgtga aagatcttct
2041 catgaatgat cggcttccag ggaaaaagac aactaaactt tgggttccag atgaagaagt
2101 atctcctgag acaatggtca aaattcaggc tattaanaatg atggttcgat ggctacttgg
2161 aatgaaaaat aatcacagta aatcaggaac ttctacctta agattgctaa caacaatatt
2221 gcatagtgat ggagacttga cagaacaggg gaaaattagt aaaccagata tgtcacgtct
2281 gagacttgct gctgggagtg ctattgtgaa gctggcacia gaaccctgtt accatgaaat
2341 catcacatta gaacaatatc agctatgtgc attagctatc aacgatgaat gctatcaagt
2401 aagacaagtg tttgccaga aacttcacia aggcctttcc cgtttacggc ttccacttga
2461 gtatatggca atctgtgccc tttgtgcaaa agatcctgta aaggagagaa gagctcatgc
2521 taggcaatgt ttggtgaaaa atataaatgt aaggcgggag tatctgaagc agcatgcagc
2581 tgttagtgaa aaattattgt ctcttctacc agagtatgtt gtccatata caattcacct
2641 tttggcacat gaccagatt atgtcaaagt acaggatatt gaacaactta aagatgttaa
2701 agaattgtct tggtttgttc tggaaatatt aatggctaaa aatgaaaata acagtcacgc
2761 ttttatcaga aagatggtag aaaatattaa acaaacaaaa gatgcccaag gaccagatga
2821 tgcaaaaatg aatgaaaaac tgtacactgt gtgtgatgtt gccatgaata tcatcatgtc
2881 aaagagtact acatacagtt tggaatctcc taaagaccgg gtactaccag ctgcttctct
2941 cactcaacct gacaagaatt tcagtaacac caaaaattat ctgctcctg aaatgaaatc
3001 atttttcact cctggaaaac ctaaaacaac caatgttcta ggagctgtta acaagccact
3061 ttcatcagca ggcaagcaat ctgagaccaa atcatcacga atggaaactg taagcaatgc
3121 aagcagcagc tcaaatccaa gctctcctgg aagaataaag gggaggcttg atagtcttga
3181 aatggatcac agtgaaaatg aagattacac aatgtcttca ccttgccgg ggaaaaaaag
3241 tgacaagaga gacgactctg atcttgtaag gtctgaattg gagaagccta gaggcaggaa
3301 aaaaacgccc gtcacagaac aggaggagaa attaggtatg gatgacttga ctaagtgtgt
3361 acaggaacag aaacctaaag gcagtcagcg aagtcggaaa agaggccata cggcttcaga
3421 atctgatgaa cagcagtggc ctgaggaaaa gaggtctcaa gaagatatat tagaaaaatg
3481 agatgaacag aatagtcgac caaaaaaggg taaaaggagg cgaccaccaa aacctcttgg
3541 tggaggtaca ccaaaagaag agccaacaat gaaaacttct aaaaaaggaa gcaaaaaaaa
3601 atctggacct ccagcaccag aggaggagga agaagaagaa agacaaagtg gaaatacgg
3661 acagaagtcc aaaagcaaac agcaccgagt gtcaaggaga gcacagcaga gagcagaatc
3721 tcctgaatct agtgcaattg aatccacaca gtccacacca cagaaaggac gaggaagacc
```

```
3781 atcaaaaacg ccatcaccat cacaaccaa aaaaaatgtg taagttgtaa atattacatt
3841 tcaaaccaat ttcaaattat ttgcaaaaag ttcctaaatt tgtaaacata catattgctg
3901 tatttaaatt ccataatatt agccccatta cactaggtac ggcggcgaag tgctaaaagg.
3961 gaacggcgat gaacaaatgt aattaataac tttctctgtg aaagccttgg aaaaatcttt
4021 tttttttttt tttttttttg gtcaagcttg aggctgaata aagcctttga tgcacaaaat
4081 gggactgctg aagagtggac agttggacct tactttggtg accccataca tttgtggtca
4141 catgctttag ccatacacat ggtaacattg actatggagt cttgtgaaag tgtaatgtgc
4201 gatggctatg tagacataaa gaagaaactt gtaaatactt tttttctttt ttttaatgtt
4261 tctgatttct gaagtgcttg tatagctttt atctgctggc ttaaaactgac agtaccgcac
4321 tgtttattgg atctattgat ttgaaaagaa tttgttagga tagatcttaa gcagtaatct
4381 gtcagtgttt gt
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Sep 16 2003 13:15:10

exon /gene="AS3"
1..46
/gene="AS3"
/number=1

exon 47..173
/gene="AS3"
/number=2

CDS 66..4241
/gene="AS3"
/codon_start=1
/product="androgen-induced prostate proliferative shutoff
associated protein"
/protein_id="AAD22134.2"
/db_xref="GI:4559410"
/translation="MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLLKMOVKTFMD
MDQDSEEEKELYLNLAHLASDFFLKHPDKDVRLLVACCLADIFRIYAPEAPYTSPPDK
LKDIFMFITRQLKGLEDTKSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRT
LFSVINNGHNQKVHMHMVDLMSSIICGDTVSQELLDTVLVNLPVPAHKNLNKQAYDLA
KALLKRTAQAIIEPYITNFFNQVLMGKTSISDLSEHVSDILELYNIDSHLLSVLPQ
LEFKLKSNDNEERLQVVKLLAKMFGAKDSELASQNKPLWQCYLGRFNDIHVPIRLECV
KFASHCLMNHDPDLAKDLTEYLKVRSHDPPEAIRHDVIVSIVTAAKKDILLVNDHLLNF
VGERTLDRWRVRKEAMMGLAQIYKKYALQSAAGKDAKQIAWIKDKLLHIYYQNSID
DRLLVERIFAQYMPVPHNLETTERMKCLYYLYATLDDLNAVKALNEMWKCQNLLRHQVKD
LLDLIKQPKTDASVKAIKFSKVMVITRSLPDGKAQDFMCKFTQVLEDEKIRKQLEVL
VSPTCCKQAEGCVREITKKLGNPKQPTNPFLEMIKFLLEIRIAPVHIDTESISALIKQ
VNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTHPISFHSAAETFESELLACLKMDDE
KVAEALQIFKNTGSKIIEEDFPHIRSALLPVLHHSKKGPPRQAKYAIHCIAIFSSK
EAQFAQIFEPLHKS LDPNLEHLITPLVTIGHIALAPDQFAAPLKS L VATFIVKDLL
MNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMKNNHKS GTS LRLRLTT
ILHSDGDLTEQ GKISKPDMSRLRLAAGSAIVKLAQEP CYHEIITLEQYQLCALAINDE
CYQVRQVFQAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQCLVKVINVRREY
LKQHAHVSEKLLSLLPEYVVPYTIHLLAHPDYVKVQDIEQLKDVKECLWFVLEILMA
KNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVCDVAMNIIMSKSTTYSLESP
KDPVLPARFFTQPDKNFSNTKNYLPPGMKSFFTPGKPKTTNVLGAVNKP LSSAGKQSQ
TKSSRMETVGNASSSSNPSSPGRIKGR L DSSEMDS ENEDYTMSSPLPGKRS DKRDDS
DLVRSELEKPRGRKKTPTVTEREEKLGMDLTKLVQEQRPKGSQRSRKRGH TASESDEQ
QWPEEKRLKEDILENEDEQNSPPKKGKRGRPPKPLGGGTPKEEPTMKTSKKGSKKSG
PPAPEEEEEERQSGNTEQKSKSQHRVSRRAQQRAESSAIESTQSTPQKGRGRP
SKTPSPSQPKKNV"

exon 174..377
/gene="AS3"
/number=3

exon 378..464
/gene="AS3"
/number=4

exon 465..562
/gene="AS3"
/number=5

exon 563..689
/gene="AS3"
/number=6

exon 690..770
/gene="AS3"
/number=7

exon 771..911
/gene="AS3"
/number=8

exon 912..1027
/gene="AS3"
/number=9

<u>exon</u>	1028..1122 /gene="AS3" /number=10
<u>exon</u>	1123..1268 /gene="AS3" /number=11
<u>exon</u>	1269..1420 /gene="AS3" /number=12
<u>exon</u>	1421..1534 /gene="AS3" /number=13
<u>exon</u>	1535..1616 /gene="AS3" /number=14
<u>exon</u>	1617..1665 /gene="AS3" /number=15
<u>exon</u>	1666..1805 /gene="AS3" /number=16
<u>exon</u>	1806..1921 /gene="AS3" /number=17
<u>exon</u>	1922..2027 /gene="AS3" /number=18
<u>exon</u>	2028..2188 /gene="AS3" /number=19
<u>exon</u>	2189..2312 /gene="AS3" /number=20
<u>exon</u>	2313..2471 /gene="AS3" /number=21
<u>exon</u>	2472..2540 /gene="AS3" /number=22
<u>exon</u>	2541..2677 /gene="AS3" /number=23
<u>exon</u>	2678..2801 /gene="AS3" /number=24
<u>exon</u>	2802..3006 /gene="AS3" /number=25
<u>exon</u>	3007..3121 /gene="AS3" /number=26
<u>exon</u>	3122..3254 /gene="AS3" /number=27
<u>exon</u>	3255..3374 /gene="AS3" /number=28
<u>exon</u>	3375..3437 /gene="AS3" /number=29

exon 3438..3583
/gene="AS3"
/number=30
exon 3584..3689
/gene="AS3"
/number=31
exon 3690..4129
/gene="AS3"
/number=32
exon 4130..4354
/gene="AS3"
/number=33
exon 4355..4810
/gene="AS3"
/number=34

BASE COUNT 1755 a 944 c 1074 g 1480 t

ORIGIN

```
1  ccggagagcc ccggagtgag cggagtagcg agtcggcaac ccggaggggt agaaatattt
61 ctgtcatggc tcattcaaag actaggacca atgatggaaa aattacatat ccgcctgggg
121 tcaaggaaat atcagataaa atatctaaag aggagatggt gagacgatta aagatggttg
181 tgaaaacttt tatggatatg gaccaggact ctgaagaaga aaaggagctt tatttaaacc
241 tagctttaca tcttgcttca gatttttttc tcaagcatcc tgataaagat gttcgcttac
301 tggtagcctg ctgccttgct gatattttca ggatttatgc tcctgaagct ccttacacat
361 cccctgataa actaaaggat atatttatgt ttataacaag acagttgaag gggctagagg
421 atacaaagag cccacagttc aataggtatt tttatttgct tgagaacatt gcttgggtca
481 agtcatataa catatgcttt gagttagaag atagcaatga aattttcacc cagctataca
541 gaaccttatt ttcagttata aacaatggcc acaatcagaa agtccatatg cacatggtag
601 accttatgag ctctattatt tgtgaagggtg atacagtgtc tcaggagctt ttggatacgg
661 ttttagtaaa tctggtacct gctcataaga atttaaaca gcaagcatat gatttggcaa
721 aggctttact gaagaggaca gctcaagcta ttgagccata tattaccaat ttttttaatc
781 aggttctgat gcttgggaaa acatctatca gcgatttgct agagcatgtc tctgacttaa
841 ttttggagct ctacaatatt gatagtcatt tgctgctctc tgttttaccc cagcttgaat
901 ttaaattaaa gagcaatgat aatgaggagc gcctacaagt tgttaaacta ctggcgaaaa
961 tgtttggggc aaaggattca gaattggctt ctcaaaacaa gccacttttg cagtgtact
1021 tgggcaggtt taatgatatc catgtaccaa tccgcctgga atgtgtgaaa tttgctagcc
1081 attgtctcat gaaccatcct gatttagcaa aagacttaac agagtatctt aaagtgaggt
1141 cacatgacct tgaggaagct attagacatg atgttattgt gtcaatagtt acagctgcta
1201 aaaaggatat tcttctggtc aatgatcact tacttaattt tgtgggagag agaacattag
1261 acaaacgatg gagagtacgc aaagaagcca tgatgggact tgcccaaatt tataagaaat
1321 atgctttaca gtcagcagct ggaaaagatg ctgcaaaaca gatagcatgg atcaaaagaca
1381 aattgctaca tataattat caaaatagta ttgatgatcg actacttggt gaacggatct
1441 ttgctcaata catggttcct cacaatttag aaactacaga acggatgaaa tgcttatatt
1501 acttgtagtc cacactggat ttaaattgctg tgaaagcatt gaatgaaatg tggaaatgtc
1561 aaaatctgct ccgacatcaa gtaaaggatt tgcttgactt gattaagcaa cccaaaacag
1621 atgccagtgt caaggccata ttttcaaaag tgatggttat tacaagaagt ttacctgac
1681 ctggttaaggc tcaggatttc atgaagaaat tcacacaggt gttagaagat gatgagaaaa
1741 taagaaagca gttagaagta cttgttagtc caacatgctc ctgcaagcag gctgaagggt
1801 gtgtgcgtga aataactaag aagttgggca accccaaaca gcctacaaat cctttcctgg
1861 aatgatcaa gtttctcttg gagaggatag cacctgtgca catagatacc gaatctatca
1921 gtgctcttat taaacaagtg aacaaatcaa tagatggaac agcagatgat gaagatgagg
1981 gtgttccaac tgatcaagcc atcagagcag gtcttgaact gcttaaggta ctctcattta
2041 cacatcccat ctcatctcat tctgctgaaa catttgaatc attactggcc tgtctgaaaa
2101 tggatgatga aaaagtagca gaagctgcac taaaaatttt caaaaacaca ggaagcaaaa
2161 ttgaagagga ttttccacac atcagatcag ccttgcttcc tgttttacat cacaaatcta
2221 aaaaaggacc ccccgctcaa gccaaatatg ccattcattg tatccatgcy atattttcta
2281 gtaaagaggc ccagtttgca cagatatttg agcctctgca taagagccta gatccaagca
2341 acctggaaca tctcataaca ccattgggtta ctattggtca tattgctctc cttgcacctg
2401 atcaatttgc tgctccttgg aaatccttgg tagtactttt cattgtgaaa gatctctcta
2461 tgaatgatcg gcttccaggg aaaaagacaa ctaaaacttg ggttccagat gaagaagtat
2521 ctctgagac aatgggtcaaa attcaggcta ttaaatgat ggttcgatgg ctacttgga
```

```
2581 tgaaaaataa tcacagtaaa tcaggaactt ctaccttaag attgctaaca acaatattgc
2641 atagtgatgg agacttgaca gaacagggga aaattagtaa accagatatg tcacgtctga
2701 gacttgctgc tgggagtgct attgtgaagc tggcacaaga accctgttac catgaaatca
2761 tcacattaga acaatatcag ctatgtgcat tagctatcaa cgatgaatgc tatcaagtaa
2821 gacaagtgtt tgcccagaaa cttcacaaaag gcctttcccg tttacggctt ccacttgagt
2881 atatggcaat ctgtgccctt tgtgcaaaaag atcctgtaaa ggagagaaga gctcatgcta
2941 ggcaatgttt ggtgaaaaat ataaatgtaa ggcgaggagta tctgaagcag catgcagctg
3001 ttagtgaaaa attattgtct cttctaccag agtatgttgt tccatataca attcaccttt
3061 tggcacatga cccagattat gtcaaagtac aggatattga acaacttaaa gatgttaaag
3121 aatgtctttg gtttgttctg gaaatattaa tggctaaaaa tgaaaaataac agtcacgctt
3181 ttatcagaaa gatggtagaa aatattaagc aaacaaaaga tgcccaagga ccagatgatg
3241 caaaaatgaa tgaaaaactg taaactgtgt gtgatgttgc catgaatc atcatgtcaa
3301 agagtactac atacagtttg gaatctccta aagaccggt actaccagct cgtttcttca
3361 ctcaacctga caagaatttc agtaacacca aaaattatct gcctcctgga atgaaatcat
3421 ttttactctc tggaacacct aaaacaacca atgttctagg agctgttaac aagccacttt
3481 catcagcagg caagcaatct cagaccaa atcatcgaat ggaaactgta ggcaatgcaa
3541 gcagcagctc aaatccaagc tctcctggaa gaataaaggg gaggcttgat agttctgaaa
3601 tggatcacag tgaaaatgaa gattacacaa tgtcttcacc tttgccgggg aaaagaagtg
3661 acaagagaga cgactctgat cttgtaaggt ctgaattgga gaagcctaga ggcagaaaaa
3721 aaacgcccgt cacagaacgg gaggagaaat taggtatgga tgacttgact aagttggtac
3781 aggaacagag acctaaaggc agtcagcgaa gtcggaagaa aggccatacg gcttcagaat
3841 ctgatgaaca gcagtggcct gaggaaaaga ggctcaaaga agatatatta gaaaatgaag
3901 atgaacagaa tagtccgcca aaaaagggtg aaagaggccg accacaaaaa cctcttggtg
3961 gaggtacacc aaaagaagag ccaacaatga aaacttctaa aaaaggaagc aaaaaaaaat
4021 ctggacctcc agcaccagag gaggaggaag aagaagaaag acaaagtgga aatacggaac
4081 agaagtccaa aagcaaacag caccgagtgt caaggagagc acagcagaga gcagaatctt
4141 ctgaatctag tgcaattgaa tccacacagt ccacaccaca gaaaggacga ggaagaccat
4201 caaaaacgcc atcaccatca caacaaaaaa aaaatgtgta agttgtaaat attacatttc
4261 aaaccaatth caaattatth tgcaaaagtt cctaaatttg taaacataca tattgctgta
4321 tttaaattcc atatatthag cccattatca ctaggtagcg cggcgaagtg ctaaaaggga
4381 acggcgatga acaaatgtaa ttaataactt tctctgtgaa agctttggaa aaatcttttt
4441 tttttttttt tttttttggt caagcttgag gctgaataaa gcctttgatg cacaaaatgg
4501 gactgctgaa gagtggacag ttggacctta ctttgggtgac ccatacatt tgtggtcaca
4561 tgcttttagc atacacatgg taacattgac tatggagtct tgtgaaagtg taatgtgcca
4621 tggctatgta gacataaaga agaaacttgt aaatatcttt tttctttttt ttaatgtttc
4681 tgattttctg agtgcttgta tagcttttat ctgcggcttt aaactgacag taccgactg
4741 tttattggat ctattgattt gaaaagaatt tgttaggata gatcttaagc agtaatctgt
4801 cagtgtttgt atttgtattt tctgcaattt tactgtgaaa aaaaatttgt tttcaacaat
4861 tgggtgtcatt ttcttgatgt cactatttgt tggagagtta aatggctctt tccctttgtg
4921 tatcttacct agtgtttact cctgggcacc cttaatcttc agaggtgcta aattgtctgc
4981 cattacacca gaaggatgcc tctgatagga ggacaacat gcaaattgtg aaatagtcct
5041 gaagtctctg gattacttta cacctcagta ttgatttgtc ccagaatttt ctggcctttc
5101 atggcaatga aaattttaag aagaaagatt taaagtattt taatttttaa gagtgtgta
5161 taaaataatg tactgaattc tttatcccat tttatcatcc tttcagtttt tattaatcta
5221 ctgtatcaat aaaattctgt aatttgaatg agt
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Sep 16 2003 13:15:10



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) 

About Entrez

Show difference in format

Entrez

Gi	Version	Update Date
4559409	2	Apr 5 1999 1:29
4539617	1	Mar 30 1999 12:03

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

LOCUS HSU95825 5253 bp mRNA linear PR1
 LOCUS HSU95825 4392 bp mRNA linear PR1
 DEFINITION Human androgen-induced prostate proliferative shutoff protein (AS3) mRNA, complete cds.

Help/FAQ

ACCESSION U95825
 VERSION U95825.2 GI:4559409
 VERSION U95825.1 GI:4539617

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 5253)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Check sequence revision history

REFERENCE 1 (bases 1 to 4392)
 AUTHORS Geck, P., Szelei, J., Jimenez, J., Soto, A.M. and Sonnenschein, C.
 TITLE Androgen-induced proliferative shutoff in prostate cancer cells: a new suppressor gene
 JOURNAL Proc. Annu. Meet. Am. Assoc. Cancer Res. 37, 223-223 (1996)
 REFERENCE 2 (bases 1 to 5253)
 REFERENCE 2 (bases 1 to 4392)

How to create WWW links to Entrez

LinkOut

AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Early gene expression during androgen-induced inhibition of proliferation of prostate cancer cells: a new suppressor gene on chromosome 13, in the BRCA2-Rb1 locus
 JOURNAL J. Steroid Biochem. Mol. Biol. 68 (1-2), 41-50 (1999)

Cubby

Related resources

MEDLINE 99229875
 PUBMED 10215036
 REFERENCE 3 (bases 1 to 5253)
 JOURNAL J. Steroid Biochem. Mol. Biol. 68, 41-45 (1999)
 REFERENCE 3 (bases 1 to 4392)

Reference sequence project

AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Anatomy and Cell Biology, Tufts Medical School, 136 Harrison Avenue, Boston, MA 02111,

LocusLink

Clusters of orthologous groups

REFERENCE 4 (bases 1 to 5253)
 AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1999) Anatomy and Cell Biology, Tufts Medical School, 136 Harrison Avenue, Boston, MA 02111,

Protein reviews on the web

REMARK Sequence update by submitter
 COMMENT On Apr 5, 1999 this sequence version replaced gi:4539617.
 COMMENT [WARNING] On Apr 5, 1999 this sequence was replaced by version gi:4559409.

FEATURES Location/Qualifiers

```

source      1..5253
source      1..4392
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /chromosome="13"
            /map="13q12-q13"
            /cell_line="LNCaP"
            /cell_type="cancer cells"
            /tissue_type="prostate"
            /note="exon 1 maps to P1 Artificial Chromosome
exons 2-24 map to cosmid 267p19; exons 25-34 r
Artificial Chromosome PAC 49J10"
gene        1..5253
            /note="exons 1-21 map to cosmid 267p19; exons
cosmid PAC49J10"
gene        1..4392
            /gene="AS3"
exon        1..46
            /gene="AS3"
            /number=1
exon        47..173
exon        47..144
            /gene="AS3"
            /number=2
CDS         66..4241
exon        145..271
            /gene="AS3"
            /number=3
CDS         170..3823
            /gene="AS3"
            /codon_start=1
            /product="androgen-induced prostate proliferat
associated protein"
            /protein_id="AAD22134.2"
            /db_xref="GI:4559410"
            /translation="MAHSKTRTNDGKITYPPGVKEISDKISKEEM
MDQDSEEEKELYLNALHLASDFFLKHPDKDVRLLVACCLADIFR
LKIDIFMFITRQLKGLEDTKSPQFNRYFYLLLENIAWVKSYNICFELI
LFSVINNGHNQKVHMHMVDLMSSIIICGDTVSQLLDTVLVNLVLP
KALLKRTAQAIIEPYITNFFNQVLMGKTSISDLSEHVSDILELYT
            /protein_id="AAD22134.1"
            /db_xref="GI:4539618"
            /translation="MHMVDLMSSIIICGDTVSQLLDTVLVNLVLP
KALLKRTAQAIIEPYITNFFNQVLMGKTSISDLSEHVFDLILELYT
LEFKLKSNDNEERLQVVKLLAKMFGAKDSELASQNKPLWQCYLGR
KFASHCLMNHPDLAKDLTEYLKVRSHDPEEAIRHDVIVSIVTAAKI
VGERTLDKRWRVRKEAMMGLAQIYKKYALQSAAGKDAKQIAWIKI
VRERTLDKRWRVRKEAMMGLAQIYKKYALQSAAGKDAKQIAWIKI
DRLLVERIFAQYMPHNLETTERMKCLYYLYATLDLNAVKALNEMV
LLDLIKQPKTDASVKAIFSKVMVITRSLPDPGKAQDFMCKFTQVLI
LLDLIKQPKTDASVKAIFSKVMVITRNLDPDPGKAQDFMCKFTQVLI
VSPTCSCKQAEGCVREITKKLGNPKQPTNPFFLEMIKFLLERIAPVI
VNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSTHPISTFHSIETI
KVAEAAALQIFKNTGSKIEEDFPHIRSALLPVLHHSKKGPPRQAK
EAQFAQIFEPLHKS LDPNLEHLITPLVTIGHIALAPDQFAAPLI
ETQFAQIFEPLHKS LDPNLEHLITPLVTIGHIALAPDQFAAPWI
MNDRLPGKKTTLKLVDPDEEVSPETMVKIQAIKMMVRWLLGMKNNH
ILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPICYHEIITLI
CYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHAR(

```

```

LKQHAADVSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDV
KNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVCDVAMNI
KDPVLPARFFTQPDKNFSNTKNYLPPGMKSFFTPGKPKTTNVLGA
TKSSRMETVGNASSSSNPSSPGRIKGRLDSSMDHSENEGYTMSSI
DLVRSELEKPRGRKKTPTVTEREEKLGMDDLTKLVQEQRPKGSQRSI
KDPVLPARFFTQPDKNFSNTKNYLPPGMKSFFTPGKPKTTNVLGA
TKSSRMETVSNASSSSNPSSPGRIKGRLDSSMDHSENEGYTMSSI
DLVRSELEKPRGRKKTPTVTEQEEKLGMDDLTKLVQEQRPKGSQRSI
QWPEEKRLKEDIENEDEQNSPPKKGKGRPPKPLGGGTPKEEPTN
PPAPEEEEEERQSGNTEQKSQKQHRVSRRAQQRASSESSAIES
PPAPEEEEEERQSGNTEQKSQKQHRVSRRAQQRASPESSAIES
SKTPSPSQPKQNV"
exon      174..377
           /gene="AS3"
           /number=3
exon      378..464
exon      272..352
           /gene="AS3"
           /number=4
exon      465..562
exon      353..493
           /gene="AS3"
           /number=5
exon      563..689
exon      494..609
           /gene="AS3"
           /number=6
exon      690..770
exon      610..704
           /gene="AS3"
           /number=7
exon      771..911
exon      705..850
           /gene="AS3"
           /number=8
exon      912..1027
exon      851..1002
           /gene="AS3"
           /number=9
exon      1028..1122
exon      1003..1116
           /gene="AS3"
           /number=10
exon      1123..1268
exon      1117..1198
           /gene="AS3"
           /number=11
exon      1269..1420
exon      1199..1247
           /gene="AS3"
           /number=12
exon      1421..1534
exon      1248..1387
           /gene="AS3"
           /number=13
exon      1535..1616
exon      1388..1503
           /gene="AS3"
           /number=14
exon      1617..1665

```

exon	1504..1609
	/gene="AS3"
	/number=15
exon	1666..1805
exon	1610..1770
	/gene="AS3"
	/number=16
exon	1806..1921
exon	1771..1894
	/gene="AS3"
	/number=17
exon	1922..2027
exon	1895..2053
	/gene="AS3"
	/number=18
exon	2028..2188
exon	2054..2122
	/gene="AS3"
	/number=19
exon	2189..2312
exon	2123..2259
	/gene="AS3"
	/number=20
exon	2313..2471
exon	2260..2383
	/gene="AS3"
	/number=21
exon	2472..2540
exon	2384..2588
	/gene="AS3"
	/number=22
exon	2541..2677
exon	2589..2703
	/gene="AS3"
	/number=23
exon	2678..2801
exon	2704..2836
	/gene="AS3"
	/number=24
exon	2802..3006
exon	2837..2956
	/gene="AS3"
	/number=25
exon	3007..3121
exon	2957..3019
	/gene="AS3"
	/number=26
exon	3122..3254
exon	3020..3165
	/gene="AS3"
	/number=27
exon	3255..3374
exon	3166..3271
	/gene="AS3"
	/number=28
exon	3375..3437
exon	3272..3711
	/gene="AS3"
	/number=29
exon	3438..3583

```

exon          3712..3936
               /gene="AS3"
               /number=30
exon          3584..3689
exon          3937..4392
               /gene="AS3"
               /number=31
exon          3690..4129
               /gene="AS3"
               /number=32
exon          4130..4354
               /gene="AS3"
               /number=33
exon          4355..4810
               /gene="AS3"
               /number=34
BASE COUNT    1755 a    944 c    1074 g    1480 t
BASE COUNT    1508 a    801 c    894 g    1189 t
ORIGIN
1  ccggagagcc ccggagttag cggagttagcg agtcggcaac ccggaggggt ag
61  ctgtcatggc tcattcaaag actaggacca atgatggaaa aattacatat cc
121  tcaaggaaat atcagataaa atattctaaag aggagatggt gagacgatta aa
181  tgaaaacttt tatggatatg gaccaggact ctgaagaaga aaaggagctt ta
241  tagctttaca tcttgcttca gatttttttc tcaagcatcc tgataaagat gt
301  tggtagcctg ctgccttgct gatattttca ggatttatgc tcctgaagct cc
361  cccctgataa actaaaggat atatttatgt ttataacaag acagttgaag gg
421  atacaaagag cccacagttc aataggtatt tttatttgct tgagaacatt gc
481  agtcatataa catatgcttt gagttagaag atagcaatga aattttcacc ca
541  gaaccttatt ttcagttata aacaatggcc acaatcagaa agtccatatg ca
601  accttatgag ctctattatt tgtgaagggtg atacagtgtc tcaggagctt tt
661  ttttagtaaa tctggtacct gctcataaga atttaaaca gcaagcatat ga
721  aggctttact gaagaggaca gctcaagcta ttgagccata tattaccaat tt
781  aggttctgat gcttgggaaa acatctatca gcgatttgct agagcatgtc tc
841  ttttgagct ctacaatatt gatagtcatt tgctgctctc tgttttaccc ca
901  ttaaattaaa gagcaatgat aatgaggagc gcctacaagt tgttaaacta ct
961  tgtttggggc aaaggattca gaattggctt ctcaaaaca gccacttttg ca
1021  tgggcagggt taatgatatc catgtaccaa tccgcctgga atgtgtgaaa tt
1081  attgtctcat gaaccatcct gatttagcaa aagacttaac agagtatctt aa
1141  cacatgaccc tgaggaagct attagacatg atgttattgt gtcaatagtt ac
1201  aaaaggatat tcttctggtc aatgatcact tacttaattt tgtgggagag ag
1261  acaaacgatg gagagtacgc aaagaagcca tgatgggact tgcccaaat ta
1321  atgctttaca gtcagcagct ggaaaagatg ctgcaaaaca gatagcatgg at
1381  aattgctaca tatatattat caaaatagta ttgatgatcg actacttggt ga
1441  ttgctcaata catggttcct cacaatttag aaactacaga acggatgaaa tq
1501  acttgatatg cacttggtat ttaaattgctg tgaaagcatt gaatgaaatg tq
1561  aaaatctgct ccgacatcaa gtaaaggatt tgcttgactt gattaagcaa cc
1621  atgccagtgt caaggccata ttttcaaaag tgatggttat tacaagaagt tt
1681  ctggttaaggc tcaggatttc atgaagaaat tcacacaggt gttagaagat ga
1741  taagaaagca gttagaagta cttgttagtc caacatgctc ctgcaagcag gc
1801  gtgtgctgta aataactaag aagttgggca accccaaaca gcctacaaat cc
1861  aatgatcaa gtttctcttg gagaggatag cacctgtgca catagatacc ga
1921  gtgctcttat taaacaagtg aacaaatcaa tagatggaac agcagatgat ga
1981  gtgttccaac tgatcaagcc atcagagcag gtcttgaaact gcttaaggta ct
2041  cacatcccat ctcatctcat tctgctgaaa catttgaaatc attactggcc tq
2101  tggatgatga aaaagtagca gaagctgcac taaaaatttt caaaaacaca gg
2161  ttgaagagga tttccacac atcagatcag ccttgcttcc tgttttacat ca
2221  aaaaaggacc ccccgtcaa gccaaatatg ccattcattg tatccatgcy at
2281  gtaaagaggc ccagtttgca cagattttg agcctctgca taagagccta ga
2341  acctggaaca tctcataaca ccattgggta ctattgggtc tattgctctc ct
2401  atcaatttgc tgctcctttg aaatcctttg tagctacttt cattgtgaaa ga

```

```

2461 tgaatgatcg gcttccaggg aaaaagacaa ctaaactttg ggttccagat ga
2521 ctccctgagac aatgggtcaaa attcaggcta ttaaaatgat ggttcgatgg ct
2581 tgaaaaataa tcacagtaaa tcagggaactt ctaccttaag attgctaaca ac
2641 atagtgatgg agacttgaca gaacagggga aaacttagtaa accagatatg tc
2701 gacttgctgc tgggagtgtt attgtgaagc tggcacaaga accctgtttac ca
2761 tcacattaga acaatatcag ctatgtgcat tagctatcaa cgatgaatgc ta
2821 gacaagtgtt tgcccagaaa cttcacaaaag gcctttcccg tttacggctt cc
2881 atatggcaat ctgtgccctt tgtgcaaaaag atcctgtaaa ggagagaaga gc
2941 ggcaatgttt ggtgaaaaat ataaatgtaa ggcgggagta tctgaagcag ca
3001 ttagtgaaaa attattgtct cttctaccag agtatgttgt tccatataca at
3061 tggcacatga cccagattat gtcaaagtac aggatattga acaacttaaa ga
3121 aatgtctttg gtttgttctg gaaatattaa tggctaaaaa tgaaaaaac ag
3181 ttatcagaaa gatggtagaa aatattaagc aaacaaaaga tgcccaagga cc
3241 caaaaatgaa tgaaaaactg tacactgtgt gtgatgttgc catgaatatc at
3301 agagtactac atacagtttg gaatctccta aagaccgggt actaccagct cc
3361 ctcaacctga caagaatttc agtaacacca aaaattatct gcctcctgga at
3421 ttttcaactcc tggaaaacct aaaacaacca atgttctagg agctgttaac aa
3481 catcagcagg caagcaatct cagaccaa atcatcgaat ggaaactgta gc
3541 gcagcagctc aaatccaagc tctcctggaa gaataaaggg gaggcttgat ag
3601 tggatcacag tgaaaatgaa gattacacaa tgtcttcacc tttgccgggg aa
3661 acaagagaga cgactctgat cttgtaaggc ctgaattgga gaagcctaga gc
3721 aaacgcccgt cacagaacgg gaggagaaat taggtatgga tgacttgact aa
3781 aggaacagag acctaaaggc agtcagcgaa gtcggaaaag aggccatacg gc
3841 ctgatgaaca gcagtggcct gaggaaaaga ggctcaaaga agatatatta ga
3901 atgaacagaa tagtccgcca aaaaagggtg aaagaggccg accaccaaaa cc
3961 gaggtacacc aaaagaagag ccaacaatga aaacttctaa aaaaggaagc aa
4021 ctggacctcc agcaccagag gagggaggaag aagaagaaag acaaagtgga aa
4081 agaagtccaa aagcaaacag caccgagtgt caaggagagc acagcagaga gc
4141 ctgaatctag tgcaattgaa tccacacagt ccacaccaca gaaaggacga gc
4201 caaaaacgcc atcaccatca caaccaaaaa aaaatgtgta agttgtaaat at
4261 aaaccaattt caaattattt tgcaaaaagt cctaaatttg taaacataca ta
4321 tttaaattcc atatatttag cccattaca ctaggtacgg cggcgaagtg ct
4381 acggcgatga acaaatgtaa ttaataactt tctctgtgaa agctttggaa aa
4441 tttttttttt tttttttggt caagcttgag gctgaataaa gcctttgatg ca
4501 gactgctgaa gagtggacag ttggacctta ctttgggtgac cccatacatt tq
4561 tgcttttagcc atacacatgg taacattgac tatggagtct tgtgaaagtg ta
4621 tggctatgta gacataaaga agaaacttgt aaatatcttt tttctttttt tt
4681 tgatttctga agtgcttgta tagcttttat ctgcggtctt aaactgacag ta
4741 tttattggat ctattgattt gaaaagaatt tgtaggata gatcttaagc ag
4801 cagtgtttgt atttgtattt tctgcaattt tactgtgaaa aaaaatttgt tt
4861 tgggtgcatt ttcttgatgt cactatttgt tggagagtta aatggctctt tc
4921 tatcttacct agtgtttact cctgggcacc cttaatcttc agagggtgcta aa
4981 cattacacca gaaggatgcc tctgatagga ggacaaccat gcaaattgtg aa
5041 gaagtctctg gattacttta cacctcagta ttgatttgtc ccagaatttt ct
5101 atggcaatga aaattttaag aagaaagatt taaagtattt taattttaaa ga
5161 taaaataatg tactgaattc tttatcccat tttatcatcc tttcagtttt ta
5221 ctgtatcaat aaaattctgt aatttgaatg agt
1 ggatacaaag agcccacaat tcaataggta tttttattta cttgagaaca tt
61 caagtcatat aacatatgct ttgagttaga agatagcaat gaaattttca cc
121 cagaacctta ttttcagtta taacaatgg ccacaatcag aaagtccata tq
181 agaccttatg agctctatta tttgtgaagg tgatacagtg tctcaggagc tt
241 ggtttttagta aatctggtac ctgctcataa gaatttaaac aagcaagcat at
301 aaaggcttta ctgaagagga cagctcaagc tattgagcca tatattacca ct
361 tcaggttctg atgcttggga aaacatctat cagcgatttg tcagagcatg tc
421 aattttggag ctctacaata ttgatagtca tttgctgctc tctgttttac cc
481 atttaaatta aagagcaatg ataatgagga gcgcctacaa gttgttaaac ta
541 aatgtttggg gcaaaggatt cagaattggc ttctcaaaac aagccacttt gc
601 cttgggcagg ttaaatgata tccatgtacc aatccgctg gaatgtgtga aa
661 ccattgtctc atgaaccatc ctgatttagc aaaagactta acagagtac tt
721 gtcacatgac cctgaggaag ctattagaca tgatgttatt gtgtcaatag tt

```



```

781 taaaaaggat attcttctgg tcaatgatca cttacttaat tttgtgagag ag
841 agacaaacga tggagagtag gcaaagaagc catgatggga cttgccccaa tt
901 atatgcttta cagtcagcag ctggaaaaga tgctgcaaaa cagatagcat gg
961 caaattgcta catatatatt atcaaaatag tattgatgat cgactacttg tt
1021 ctttgtctcaa tacatggttc ctccacaattt agaaactaca gaacggatga aa
1081 ttacttgtat gccacactgg atttaaattgc tgtgaaagca ttgaatgaaa tg
1141 tcaaaatctg ctccgacatc aagtaaagga tttgcttgac ttgattaagc aa
1201 agatgccagt gtcaaggcca ttttttcaaa agtgatgggtt attacaagaa at
1261 tcctggtaag gctcaggatt tcatgaagaa attcacacag gtgttagaag at
1321 aataagaaag cagttagaag tacttgtagg tccaacatgc tcctgcaagc ag
1381 ttgtgtgcgt gaaataacta agaagttggg caacccccaa cagcctacaa at
1441 ggaaatgatc aagtttctct tggagaggat agcacctgtg cacatagata cc
1501 cagtgtctct attaaacaag tgaacaaatc aatagatgga acagcagatg at
1561 ggggtgttcca actgatcaag ccatcagagc aggtcttgaa ctgcttaagg ta
1621 tacacatccc atctcatttc attctgctga aacatttgaa tcattactgg ct
1681 aatggatgat gaaaaagtag cagaagctgc actacaaatt ttcaaaaaca ca
1741 aattgaagag gattttccac acatcagatc agccttgctt cctgttttac at
1801 taaaaaagga ccccccgctc aagccaaata tgccattcat tgtatccatg cc
1861 tagtaaagag acccagtttg cacagatatt tgagcctctg cataagagcc ta
1921 caacctggaa catctcataa caccattggg tactattggg catattgctc tc
1981 tgatcaattt gctgctcctt ggaaatcctg ggtagctact ttcattgtga aa
2041 catgaatgat cggcttccag ggaaaaagac aactaaactt ttgggtccag at
2101 atctcctgag acaatggcca aaattcaggc tattaaaatg atgggtccag gg
2161 aatgaaaaat aatcacagta aatcaggaac ttctacctta agattgctaa ca
2221 gcatagtgat ggagacttga cagaacaggg gaaaattagt aaaccagata tg
2281 gagacttgct gctgggagtg ctattgtgaa gctggcaca gaacctgtt ac
2341 catcacatta gaacaatata agctatgtgc attagctatc aacgatgaat gc
2401 aagacaagtg tttgcccaga aacttcacaa aggcctttcc cgtttacggc tt
2461 gtatatggca atctgtgccc tttgtgcaaa agatcctgta aaggagagaa ga
2521 taggcaatgt ttggtgaaaa atataaatgt aaggcgggag tatctgaagc ag
2581 tgttagtgaa aaattattgt ctcttctacc agagtatgtt gttccatata ca
2641 tttggcacat gaccagatt atgtcaaagt acaggatatt gaacaactta aa
2701 agaatgtctt tggtttggtc tggaaatatt aatggctaaa aatgaaaata ac
2761 ttttatcaga aagatggtag aaaatatata acaaacaaaa gatgcccag ga
2821 tgcaaaaatg aatgaaaaac tgtacactgt gtgtgatgtt gccatgaata tc
2881 aaagagtact acatacagtt tggaaatctc taaagaccgc gtactaccag ct
2941 cactcaacct gacaagaatt tcagtaacac caaaaattat ctgcctcctg aa
3001 atttttcact cctggaaaac ctaaaacaac caatgttcta ggagctgtta ac
3061 ttcacagca ggcaagcaat ctgacccaa atcatcacga atggaaaactg ta
3121 aagcagcagc tcaaatccaa gctctcctgg aagaataaag gggaggcttg at
3181 aatggatcac agtgaaaatg aagattacac aatgtcttca cctttgcccgg gg
3241 tgacaagaga gacgactctg atcttgtaag gtctgaattg gagaagccta ga
3301 aaaaacgccc gtcacagaac agggaggagaa attaggtatg gatgacttga ct
3361 acaggaacag aaacctaaag gcagtcagcg aagtcggaaa agaggccata cc
3421 atctgatgaa cagcagtggc ctgaggaaaa gaggtcaaaa gaagatatat ta
3481 agatgaacag aatagtccgc caaaaaaggg taaaagaggc cgaccacca aa
3541 tggaggtaca ccaaaagaag agccaacaat gaaaacttct aaaaaaggaa gc
3601 atctggacct ccagcaccag agggaggagga agaagaagaa agacaaagtg ga
3661 acagaagtcc aaaagcaaac agcaccgagt gtcaaggaga gcacagcaga ga
3721 tcctgaatct agtgcaattg aatccacaca gtccacacca cagaaaggac ga
3781 atcaaaaacg ccatcaccat cacaacccaa aaaaaatgtg taagttgtaa at
3841 tcaaaccaat ttcaaattat tttgcaaaag ttcttaaatt tgtaaacata ca
3901 tatttaaatt ccatatattt agccccatta cactaggtac ggcggcgaag tg
3961 gaacggcgat gaacaaatgt aattaataac tttctctgtg aaagcttttg aa
4021 tttttttttt tttttttttg gtcaagcttg aggtgaata aagcctttga tg
4081 gggactgctg aagagtggac agttggacct tactttgggtg accccatata tt
4141 catgctttag ccatacacat ggtaacattg actatggagt cttgtgaaag tg
4201 gatggctatg tagacataaa gaagaaactt gtaaatatct ttttctttt tt
4261 tctgatttct gaagtgtctg tatagctttt atctgcggct ttaaactgac ag
4321 tgtttatttg atctattgat ttgaaaagaa tttgttagga tagatcttaa gc

```

4381 gtcagtgttt gt
//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style Seqlds) 

About Entrez

Show difference in format

Entrez

Gi	Version	Update Date
4559409	2	Apr 5 1999 1:29
4539617	1	Mar 30 1999 12:03

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Number of accessions to be compared: Old = 1, New = 1

Number of matched accessions: 1

Number of unmatched accessions: Old = 0, New = 0

Help|FAQ

Accession = U95825, Locus = HSU95825

=====

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

Differences in LOCUS names:

old: "LOCUS	HSU95825	4392 bp	mRNA	linear
-------------	----------	---------	------	--------

Check sequence revision history

	30-MAR-1999"			
new: "LOCUS	HSU95825	5253 bp	mRNA	linear

05-APR-1999"

How to create WWW links to Entrez

Differences in VERSION:

LinkOut

old: "U95825.1 GI:4539617"

Cubby

new: "U95825.2 GI:4559409"

Differences in BASECOUNT:

Related resources

old: " 1508 a 801 c 894 g 1189 t"

BLAST

new: " 1755 a 944 c 1074 g 1480 t"

Reference sequence project

Differences in COMMENT:

LocusLink

old: "[WARNING] On Apr 5, 1999 this sequence was replaced by a new

Clusters of orthologous groups

gi:4559409."

new: "On Apr 5, 1999 this sequence version replaced gi:4539617."

Protein reviews on the web

Differences in SEQUENCE:

First base with diff: 1
 The number of diffs: 3245
 Old length: 4392
 New length: 5253

Threshold: 10

Bases with diffs: 1, 2, 3, 4, 6, 8, 9, 10, 11

Differences in FEATURE.source:

```
-----
Old feature      source      1..4392
                  /note              = "exons 1-21 map to cosmid 267p19;
                               22-31 map to cosmid PAC49J10"
                  /organism         = "Homo sapiens"
                  /mol_type          = "mRNA"
                  /db_xref           = "taxon:9606"
                  /chromosome        = "13"
                  /map               = "13q12-q13"
                  /cell_line         = "LNCaP"
                  /cell_type         = "cancer cells"
                  /tissue_type       = "prostate"
```

Differences in FEATURE.gene:

```
-----
Old feature      gene        1..4392
                  /gene              = "AS3"
```

Differences in FEATURE.exon:

```
-----
Old feature      exon        47..144
                  /gene              = "AS3"
                  /number            = "2"
```

Differences in FEATURE.exon:

```
-----
Old feature      exon        145..271
                  /gene              = "AS3"
                  /number            = "3"
```

Differences in FEATURE.CDS:

```
-----
Old feature      CDS          170..3823
                  /gene              = "AS3"
                  /codon_start        = "1"
                  /product            = "androgen-induced prostate prolifer-
                               shutoff associated protein"
                  /protein_id         = "AAD22134.1"
                  /db_xref            = "GI:4539618"
                  /translation        = "MHMV DLMSSII CEGDTVSQELLDTVLVNLVPA
AKALLKRTAQAI EPYITTFNQVLM LGKTSIS
ELYNIDSHLLLSVLPQLEFKLSNDNEERLQV
DSELASQNKPLWQCYLGRFNDIHVPIRLECVI
LAKDLTEY LKVRSHDPEEAI RHDVIVSIVTA
LNFVRERTLDKRWRVRKEAMMGLAQIYKKYAI
IAWIKDKLLHIYYQNSIDRLLVERIFAQYMA
CLYYLYATLDLNAV KALNEMWKCQNLLRHQVI
DASVKAIFSKVMVITRNLPDPGKAQDFMCKF
QLEVLVSPTCSCQAEGCVREITKKLG NPKQI
LERIAPVHIDTESISALIKQVNKSIDGTADDI
AGLELLKVLSFTHPI SFHSAETFESLLACLKN
IFKNTGSKIEEDFPHIRSALLPVLHHSKKG I
HAIFSSKETQFAQIF EPLHKS LDP SNLEHLIT
APDQFAAPWKS WVATFIVKDLLMNDRLPGKKI
PETMVKIQA IKMMVRWLLGMKNHNSKSGTSTI
DLTEQ GKISKPDMSRLRLAAGSAIVKLAQEP"
```

LCALAINDECYQVRQVFAQKLHKGLSRLRLPI
 DPVKERRAHARQCLVKININVRREYLKQHAAV
 VPYTIHLLAHDPDYVKVQDIEQLKDVKECLW
 NSHAFIRKMVENIKQTKDAQGPDDAKMNEKL
 SKSTTYSLESPKDPVLPARFFTQPDKNFSNTI
 TPGKPKTTNVLGAVNKPLSSAGKQSQTSSRI
 PSSPGRIKGRLDSEMDHSENYDTMSSPLPC
 VRSELEKPRGRKKTPTVTEQEEKLGMDDLTKL
 RKRGHASESEDEQQWPPEEKRLKEDILENEDE
 PPKPLGGGTPKEEPTMKTSKKGSKKSGPPAI
 NTEQSKSKQHRVSRRAQRAESPESAIEST
 SKTPSPSQPKQNV"

Differences in FEATURE.exon:

 Old feature exon 272..352
 /gene = "AS3"
 /number = "4"

Differences in FEATURE.exon:

 Old feature exon 353..493
 /gene = "AS3"
 /number = "5"

Differences in FEATURE.exon:

 Old feature exon 494..609
 /gene = "AS3"
 /number = "6"

Differences in FEATURE.exon:

 Old feature exon 610..704
 /gene = "AS3"
 /number = "7"

Differences in FEATURE.exon:

 Old feature exon 705..850
 /gene = "AS3"
 /number = "8"

Differences in FEATURE.exon:

 Old feature exon 851..1002
 /gene = "AS3"
 /number = "9"

Differences in FEATURE.exon:

 Old feature exon 1003..1116
 /gene = "AS3"
 /number = "10"

Differences in FEATURE.exon:

 Old feature exon 1117..1198
 /gene = "AS3"
 /number = "11"

Differences in FEATURE.exon:

Old feature exon 1199..1247
 /gene = "AS3"
 /number = "12"

Differences in FEATURE.exon:

Old feature exon 1248..1387
 /gene = "AS3"
 /number = "13"

Differences in FEATURE.exon:

Old feature exon 1388..1503
 /gene = "AS3"
 /number = "14"

Differences in FEATURE.exon:

Old feature exon 1504..1609
 /gene = "AS3"
 /number = "15"

Differences in FEATURE.exon:

Old feature exon 1610..1770
 /gene = "AS3"
 /number = "16"

Differences in FEATURE.exon:

Old feature exon 1771..1894
 /gene = "AS3"
 /number = "17"

Differences in FEATURE.exon:

Old feature exon 1895..2053
 /gene = "AS3"
 /number = "18"

Differences in FEATURE.exon:

Old feature exon 2054..2122
 /gene = "AS3"
 /number = "19"

Differences in FEATURE.exon:

Old feature exon 2123..2259
 /gene = "AS3"
 /number = "20"

Differences in FEATURE.exon:

Old feature exon 2260..2383
 /gene = "AS3"
 /number = "21"

Differences in FEATURE.exon:

Old feature exon 2384..2588
 /gene = "AS3"
 /number = "22"

Differences in FEATURE.exon:

Old feature exon 2589..2703
 /gene = "AS3"
 /number = "23"

Differences in FEATURE.exon:

Old feature exon 2704..2836
 /gene = "AS3"
 /number = "24"

Differences in FEATURE.exon:

Old feature exon 2837..2956
 /gene = "AS3"
 /number = "25"

Differences in FEATURE.exon:

Old feature exon 2957..3019
 /gene = "AS3"
 /number = "26"

Differences in FEATURE.exon:

Old feature exon 3020..3165
 /gene = "AS3"
 /number = "27"

Differences in FEATURE.exon:

Old feature exon 3166..3271
 /gene = "AS3"
 /number = "28"

Differences in FEATURE.exon:

Old feature exon 3272..3711
 /gene = "AS3"
 /number = "29"

Differences in FEATURE.exon:

Old feature exon 3712..3936
 /gene = "AS3"
 /number = "30"

Differences in FEATURE.exon:

Old feature exon 3937..4392
 /gene = "AS3"
 /number = "31"

Differences in FEATURE.source:

```

-----
New feature      source      1..5253
                  /note              = "exon 1 maps to P1 Artificial Chr
                                PAC26H23; exons 2-24 map to cosm
                                exons 25-34 map to P1 Artificial
                                Chromosome PAC 49J10"
                  /organism          = "Homo sapiens"
                  /mol_type          = "mRNA"
                  /db_xref           = "taxon:9606"
                  /chromosome        = "13"
                  /map               = "13q12-q13"
                  /cell_line         = "LNCaP"
                  /cell_type         = "cancer cells"
                  /tissue_type       = "prostate"

```

Differences in FEATURE.gene:

```

-----
New feature      gene        1..5253
                  /gene              = "AS3"

```

Differences in FEATURE.exon:

```

-----
New feature      exon        47..173
                  /gene              = "AS3"
                  /number            = "2"

```

Differences in FEATURE.CDS:

```

-----
New feature      CDS         66..4241
                  /gene              = "AS3"
                  /codon_start       = "1"
                  /product            = "androgen-induced prostate proli
                                shutoff associated protein"
                  /protein_id        = "AAD22134.2"
                  /db_xref           = "GI:4559410"
                  /translation       = "MAHSKTRTNDGKITYPGPKVEISDKISKEEM
                                DMDQDSEEEKELYLNLAHLASDFFLKHPDKI
                                IFRIYAPEAPYTS PDKLKDIFMFITRQLKGLF
                                YLLENIAWVKSYNICEFELEDSNEIFTQLYRTI
                                VHMHMVDLMSSIIICEGDTSVQELLDTVLVNLV
                                DLAKALLKRTAQAI EPYITNFFNQVLMLGKTS
                                ILELYNIDSHLLLSVLPQLEFKLKSNDNEERI
                                AKDSELASQNKPLWQCYLGRFNDIHVPIRLE
                                PDLAKDLTEYLKVRSHDPEEAIRHDVIVSIV
                                HLLNFVVGERTLDKRWRVRKEAMMGLAQIYKK
                                KQIAWIKDKLLHIYYQNSIDDRLLVERIFAQ
                                MKCLYYLYATLDLNAVKALNEMWKCQNLLRH
                                KTDASVKAI FSKVMVITRSLPDPGKAQDFMK
                                RKQLEVLVSP TCSCKQAEGCVREITKKLGNP
                                FLLERIAPVHIDTESISALIKQVNKSIDGTAI
                                IRAGLELLKVLSFTHPI SFHSAETFESLLACI
                                LQIFKNTGSKIEEDFPHIRSALLPVLHHKSKI
                                CIHAIFSSKEAQFAQIFEPLHKSLDPSNLEHI
                                LLAPDQFAAPLKS LVATFIVKDLLMNDRLPGI
                                VSPETMVKIQA I KMMVRWLLGMKNHNSKSGT
                                DGDLTEQ GKISKPDMSRLRLAAGSAIVKLAQ
                                YQLCALAINDECYQVRQVFAQKLHKGLSRLRI
                                AKDPVKERRAHARQCLVKININVRREYLKQHA

```


YVVPYTIHLLAHPDYVKVQDIEQLKDVKECI
 ENNSHAFIRKMVENIKQTKDAQGPDDAKMNEI
 IMSKSTTYSLESPKDPVLPARFFTQPDKNFSI
 FFTPGKPKTTNVLGAVNKPPLSSAGKQSQTKE
 SNPSSPGRIKGRLDSSMDHSENYDTMSSPI
 DLVRSELEKPRGRKKTPTVTEREEKLGMDDLTI
 RSRKRGHRTASESDEQQWPPEEKRLKEDIENEI
 GRPPKPLGGGTPKEPTMKTSKKGSKKSGPI
 SGNTEQKSKSKQHRVSRRAQQRAESSSAII
 RPSKTPSPSQPKNV"

Differences in FEATURE.exon:

 New feature exon 174..377
 /gene = "AS3"
 /number = "3"

Differences in FEATURE.exon:

 New feature exon 378..464
 /gene = "AS3"
 /number = "4"

Differences in FEATURE.exon:

 New feature exon 465..562
 /gene = "AS3"
 /number = "5"

Differences in FEATURE.exon:

 New feature exon 563..689
 /gene = "AS3"
 /number = "6"

Differences in FEATURE.exon:

 New feature exon 690..770
 /gene = "AS3"
 /number = "7"

Differences in FEATURE.exon:

 New feature exon 771..911
 /gene = "AS3"
 /number = "8"

Differences in FEATURE.exon:

 New feature exon 912..1027
 /gene = "AS3"
 /number = "9"

Differences in FEATURE.exon:

 New feature exon 1028..1122
 /gene = "AS3"
 /number = "10"

Differences in FEATURE.exon:

New feature exon 1123..1268
 /gene = "AS3"
 /number = "11"

Differences in FEATURE.exon:

New feature exon 1269..1420
 /gene = "AS3"
 /number = "12"

Differences in FEATURE.exon:

New feature exon 1421..1534
 /gene = "AS3"
 /number = "13"

Differences in FEATURE.exon:

New feature exon 1535..1616
 /gene = "AS3"
 /number = "14"

Differences in FEATURE.exon:

New feature exon 1617..1665
 /gene = "AS3"
 /number = "15"

Differences in FEATURE.exon:

New feature exon 1666..1805
 /gene = "AS3"
 /number = "16"

Differences in FEATURE.exon:

New feature exon 1806..1921
 /gene = "AS3"
 /number = "17"

Differences in FEATURE.exon:

New feature exon 1922..2027
 /gene = "AS3"
 /number = "18"

Differences in FEATURE.exon:

New feature exon 2028..2188
 /gene = "AS3"
 /number = "19"

Differences in FEATURE.exon:

New feature exon 2189..2312
 /gene = "AS3"
 /number = "20"

Differences in FEATURE.exon:

New feature exon 2313..2471
 /gene = "AS3"
 /number = "21"

Differences in FEATURE.exon:

New feature exon 2472..2540
 /gene = "AS3"
 /number = "22"

Differences in FEATURE.exon:

New feature exon 2541..2677
 /gene = "AS3"
 /number = "23"

Differences in FEATURE.exon:

New feature exon 2678..2801
 /gene = "AS3"
 /number = "24"

Differences in FEATURE.exon:

New feature exon 2802..3006
 /gene = "AS3"
 /number = "25"

Differences in FEATURE.exon:

New feature exon 3007..3121
 /gene = "AS3"
 /number = "26"

Differences in FEATURE.exon:

New feature exon 3122..3254
 /gene = "AS3"
 /number = "27"

Differences in FEATURE.exon:

New feature exon 3255..3374
 /gene = "AS3"
 /number = "28"

Differences in FEATURE.exon:

New feature exon 3375..3437
 /gene = "AS3"
 /number = "29"

Differences in FEATURE.exon:

New feature exon 3438..3583
 /gene = "AS3"
 /number = "30"

Differences in FEATURE.exon:

```

-----
New feature      exon      3584..3689
                  /gene          = "AS3"
                  /number       = "31"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      3690..4129
                  /gene          = "AS3"
                  /number       = "32"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      4130..4354
                  /gene          = "AS3"
                  /number       = "33"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      4355..4810
                  /gene          = "AS3"
                  /number       = "34"

```

Differences in REFERENCE:

Old reference:

```

      refline:      "2 (bases 1 to 4392)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnensche
                    Soto,A.M."
      title:         "Early gene expression during androgen-indu
                    inhibition of proliferation of prostate ca
                    cells: a new suppressor candidate on chrom
                    in the BRCA2-Rb1 locus"
      journal:       "J. Steroid Biochem. Mol. Biol. 68, 41-45"

```

New reference:

```

      refline:      "2 (bases 1 to 5253)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnensche
                    Soto,A.M."
      title:         "Early gene expression during androgen-indu
                    inhibition of proliferation of prostate ca
                    cells: a new suppressor candidate on chrom
                    in the BRCA2-Rb1 locus"
      journal:       "J. Steroid Biochem. Mol. Biol. 68 (1-2), 4
      muid:          "99229875"
      pmid:          "10215036"

```

New reference:

```

      refline:      "4 (bases 1 to 5253)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnensche
                    Soto,A.M."
      title:         "Direct Submission"
      journal:       "Submitted (05-APR-1999) Anatomy and Cell I
                    Tufts University Medical School, 136 Harri
                    Avenue, Boston, MA 02111, USA"
      remark:        "Sequence update by submitter"

```

Differences in ORGANISM:

Changed lineage =

```

      old: "Eukaryota; Metazoa; Chordata; Craniata; Verte
          Mammalia; Eutheria; Primates; Catarrhini; Hom

```

^
Homo."
new: "Eukaryota; Metazoa; Chordata; Craniata; Verte
Euteleostomi; Mammalia; Eutheria; Primates; C
^
Hominidae; Homo."

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds)



About Entrez

Show difference in format

	Gi	Version	Update Date
Entrez	4559409	2	Apr 5 1999 1:29
Search for Genes	4539617	1	Mar 30 1999 12:03

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Query= gi|4559409|gb|U95825.2|HSU95825 Human androgen-induced prostatic proliferative shutoff associated protein (AS3) mRNA, complete cds (5253 letters)

Help/FAQ

<gi|4539617|gb|U95825.1|HSU95825 Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds
Length = 4392

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

Score = 7583 bits (3825), Expect = 0.0
Identities = 3959/4017 (98%)
Strand = Plus / Plus

Check sequence revision history

Query: 419 ggatacaaaagagccacagttcaataggtatttttatttgcttgagaacattgct
Sbjct: 1 ggatacaaaagagccacaattcaataggtatttttatttacttgagaacattgct

How to create WWW links to Entrez

Query: 479 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcaccca
Sbjct: 61 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcaccca

LinkOut

Cubby

Query: 539 cagaaccttattttcagttataaacaatggccacaatcagaaagtcctatgca
Sbjct: 121 cagaaccttattttcagttataaacaatggccacaatcagaaagtcctatgca

Related resources

BLAST

Query: 599 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt
Sbjct: 181 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt

Reference sequence project

LocusLink

Query: 659 ggtttttagtaaatctggtacctgctcataagaatttaacaagcaagcatatgat
Sbjct: 241 ggtttttagtaaatctggtacctgctcataagaatttaacaagcaagcatatgat

Clusters of orthologous groups

Protein reviews on the web

Query: 719 aaaggctttactgaagaggacagctcaagctattgagccatatattaccaannr
Sbjct: 301 aaaggctttactgaagaggacagctcaagctattgagccatatattaccactttt

Query: 779 tcaggttctgatgcttgggaaaacatctatcagcgatttgcagagcatgtctct

```
|||||
Sbjct: 361 tcaggttctgatgcttgggaaaacatctatcagcgatttgctcagagcatgtcttt

Query: 839 aattttggagctctacaatattgatagtcatttgctgctctctgttttaccac
|||||
Sbjct: 421 aattttggagctctacaatattgatagtcatttgctgctctctgttttaccac

Query: 899 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactactg
|||||
Sbjct: 481 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactactg

Query: 959 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggcac
|||||
Sbjct: 541 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggcac

Query: 1019 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaattt
|||||
Sbjct: 601 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaattt

Query: 1079 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa
|||||
Sbjct: 661 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa

Query: 1139 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac
|||||
Sbjct: 721 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac

Query: 1199 taaaaaggatattcttctggtcaatgatcacttacttaattttgtgggagagaga
|||||
Sbjct: 781 taaaaaggatattcttctggtcaatgatcacttacttaattttgtggagagagaga

Query: 1259 agacaaacgatggagagtacgcaaagaagccatgatgggacttgcccaaatttat
|||||
Sbjct: 841 agacaaacgatggagagtacgcaaagaagccatgatgggacttgcccaaatttat

Query: 1319 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggatc
|||||
Sbjct: 901 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggatc

Query: 1379 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa
|||||
Sbjct: 961 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa

Query: 1439 ctttgctcaatacatggttcctcacaatttagaaactacagaacggatgaaatgc
|||||
Sbjct: 1021 ctttgctcaatacatggttcctcacaatttagaaactacagaacggatgaaatgc

Query: 1499 ttacttgtagccacactggatttaaatgctgtgaaagcattgaatgaaatgtgc
```

Sbjct: 1081 ttacttgatgcccactggatttaaagctgtgaaagcattgaatgaaatgtg

Query: 1559 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc

Sbjct: 1141 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc

Query: 1619 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaagttt

Sbjct: 1201 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaattt

Query: 1679 tcctggtaaggctcaggatttcatgaagaaattcacacagggtgttagaagatgat

Sbjct: 1261 tcctggtaaggctcaggatttcatgaagaaattcacacagggtgttagaagatgat

Query: 1739 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct

Sbjct: 1321 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct

Query: 1799 ttgtgtgctgaaataactaagaagttgggcaaccccaaacagcctacaaatcct

Sbjct: 1381 ttgtgtgctgaaataactaagaagttgggcaaccccaaacagcctacaaatcct

Query: 1859 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga

Sbjct: 1441 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga

Query: 1919 cagtgtcttattaacaagtgaacaaatcaatagatggaacagcagatgatga

Sbjct: 1501 cagtgtcttattaacaagtgaacaaatcaatagatggaacagcagatgatga

Query: 1979 ggggtgtccaactgatcaagccatcagagcaggctctgaactgcttaaggctact

Sbjct: 1561 ggggtgtccaactgatcaagccatcagagcaggctctgaactgcttaaggctact

Query: 2039 tacacatcccatctcatttcattctgctgaaacatttgaatcattactggcctgt

Sbjct: 1621 tacacatcccatctcatttcattctgctgaaacatttgaatcattactggcctgt

Query: 2099 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg

Sbjct: 1681 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg

Query: 2159 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca

Sbjct: 1741 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca

Query: 2219 taaaaaaggannnnnnngtcaagccaaatatgccattcattgtatccatgcgat

Sbjct: 1801 taaaaaaggacccccccgtcaagccaaatatgccattcattgtatccatgcgata
Query: 2279 tagtaaagaggcccagtttgacagatatattgagcctctgcataagagcctagat
Sbjct: 1861 tagtaaagagaccagtttgacagatatattgagcctctgcataagagcctagat
Query: 2339 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Sbjct: 1921 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Query: 2399 tgatcaatttgctgctcctttgaaatccttggtagctactttcattgtgaaagat
Sbjct: 1981 tgatcaatttgctgctcctttggaaatccttggtagctactttcattgtgaaagat
Query: 2459 catgaatgatcggcttccagggaaaaagacaactaaactttgggttccagatgaa
Sbjct: 2041 catgaatgatcggcttccagggaaaaagacaactaaactttgggttccagatgaa
Query: 2519 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Sbjct: 2101 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Query: 2579 aatgaaaaataatcacagtaaatacaggaacttctaccttaagattgctaacaaca
Sbjct: 2161 aatgaaaaataatcacagtaaatacaggaacttctaccttaagattgctaacaaca
Query: 2639 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Sbjct: 2221 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Query: 2699 gagacttgctgctgggagtgctattgtgaagctggcacaagaaccctgttaccat
Sbjct: 2281 gagacttgctgctgggagtgctattgtgaagctggcacaagaaccctgttaccat
Query: 2759 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Sbjct: 2341 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Query: 2819 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Sbjct: 2401 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Query: 2879 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Sbjct: 2461 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Query: 2939 taggcaatggttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat

Sbjct: 2521 taggcaatgtttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat

Query: 2999 tgtagtgaaaaattattgtctcttctaccagagtattgtgttccatatacaatt
|||||

Sbjct: 2581 tgtagtgaaaaattattgtctcttctaccagagtattgtgttccatatacaatt

Query: 3059 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
|||||

Sbjct: 2641 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat

Query: 3119 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
|||||

Sbjct: 2701 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt

Query: 3179 ttttatcagaaagatggtagaaaatattaagcaaaacaaaagatgcccaaggacca
|||||

Sbjct: 2761 ttttatcagaaagatggtagaaaatattaagcaaaacaaaagatgcccaaggacca

Query: 3239 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
|||||

Sbjct: 2821 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc

Query: 3299 aaagagtactacatacagtttggaatctcctaagacccgggtactaccagctcgt
|||||

Sbjct: 2881 aaagagtactacatacagtttggaatctcctaagacccgggtactaccagctcgt

Query: 3359 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctggaatc
|||||

Sbjct: 2941 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctggaatc

Query: 3419 atttttcactcctggaaaacctaacaacccaatgttctaggagctgttaacaac
|||||

Sbjct: 3001 atttttcactcctggaaaacctaacaacccaatgttctaggagctgttaacaac

Query: 3479 ttcatacagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc
|||||

Sbjct: 3061 ttcatacagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc

Query: 3539 aagcagcagctcaaatacaagctctcctggaagaataaaggggaggcttgatagt
|||||

Sbjct: 3121 aagcagcagctcaaatacaagctctcctggaagaataaaggggaggcttgatagt

Query: 3599 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa
|||||

Sbjct: 3181 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa

Query: 3659 tgacaagagagacgactctgatcttgtaagggtctgaattggagaagcctagaggc

Sbjct: 3241 |||tgacaagagagacgactctgatcttgtaagggtctgaattggagaagcctagaggc

Query: 3719 nnnnnncgcccgtcacagaacgggaggagaaattaggtatggatgacttgactaac
|||

Sbjct: 3301 aaaaacgcccgtcacagaacaggaggagaaattaggtatggatgacttgactaac

Query: 3779 acaggaacagagacctaagggcagtcagcgaagtcggaaaagaggccatacggct
|||

Sbjct: 3361 acaggaacagaaacctaagggcagtcagcgaagtcggaaaagaggccatacggct

Query: 3839 atctgatgaacagcagtggtcctgaggaaaagaggctcaaagaagatatattaga
|||

Sbjct: 3421 atctgatgaacagcagtggtcctgaggaaaagaggctcaaagaagatatattaga

Query: 3899 agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccaccaaaccct
|||

Sbjct: 3481 agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccaccaaaccct

Query: 3959 tggagggtacaccaaagaagagccaacaatgaaaacttctaaaaaaggaagcnnr
|||

Sbjct: 3541 tggagggtacaccaaagaagagccaacaatgaaaacttctaaaaaaggaagcaaa

Query: 4019 ntctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat
|||

Sbjct: 3601 atctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat

Query: 4079 acagaagtcctaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagca
|||

Sbjct: 3661 acagaagtcctaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagca

Query: 4139 ttctgaatctagtgaattgaatccacacagtcacaccacagaaaggacgagg
|||

Sbjct: 3721 tcctgaatctagtgaattgaatccacacagtcacaccacagaaaggacgagg

Query: 4199 atcaaaaacgccatcaccatcacaaccnnnnnnntgtgtaagttgtaaatatt
|||

Sbjct: 3781 atcaaaaacgccatcaccatcacaaccnaaaatgtgtaagttgtaaatatt

Query: 4259 tcaaaccaatttcaaattattttgcaaaaagttcctaaatttgtaaacatacatat
|||

Sbjct: 3841 tcaaaccaatttcaaattattttgcaaaaagttcctaaatttgtaaacatacatat

Query: 4319 tatttaaatccatatatttagccccattacactaggtacggcggcgaagtgtc
|||

Sbjct: 3901 tatttaaatccatatatttagccccattacactaggtacggcggcgaagtgtc

Query: 4379 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaa

|||||
Sbjct: 3961 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaaa

Score = 396 bits (200), Expect = e-113
Identities = 200/200 (100%)
Strand = Plus / Plus

Query: 4458 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga
|||||
Sbjct: 4040 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

Query: 4518 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat
|||||
Sbjct: 4100 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

Query: 4578 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga
|||||
Sbjct: 4160 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga

Query: 4638 agaagaaacttgtaaataatc 4657
|||||
Sbjct: 4220 agaagaaacttgtaaataatc 4239

Score = 274 bits (138), Expect = 7e-76
Identities = 138/138 (100%)
Strand = Plus / Plus

Query: 4673 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga
|||||
Sbjct: 4255 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga

Query: 4733 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta
|||||
Sbjct: 4315 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta

Query: 4793 taatctgtcagtgtttgt 4810
|||||
Sbjct: 4375 taatctgtcagtgtttgt 4392

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 1943 caaatcaatagat 1955
|||||
Sbjct: 4343 caaatcaatagat 4331

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 4749 atctattgatttg 4761
 |||||
Sbjct: 1537 atctattgatttg 1525

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 718 caaaggcttta 728
 |||||
Sbjct: 4069 caaaggcttta 4059

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2384 tgctctccttg 2394
 |||||
Sbjct: 3703 tgctctccttg 3693

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 5118 aagaagaaaga 5128
 |||||
Sbjct: 3633 aagaagaaaga 3643

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2307 tttgagcctct 2317
 |||||
Sbjct: 3460 tttgagcctct 3450

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)

Strand = Plus / Minus

Query: 1079 ccattgtctca 1089
 |||||
Sbjct: 2117 ccattgtctca 2107

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 637 tgtctcaggag 647
 |||||
Sbjct: 2113 tgtctcaggag 2103

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4111 caaggagagca 4121
 |||||
Sbjct: 1976 caaggagagca 1966

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3868 agaggctcaaa 3878
 |||||
Sbjct: 1899 agaggctcaaa 1889

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2148 acaggaagcaa 2158
 |||||
Sbjct: 1785 acaggaagcaa 1775

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2193 ttgcttctgt 2203
 |||||

Sbjct: 1740 ttgcttcctgt 1730

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 353 ttacacatccc 363
 |||||
Sbjct: 1620 ttacacatccc 1630

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 5069 tattgatttgt 5079
 |||||
Sbjct: 1534 tattgatttgt 1524

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2525 tgagacaatgg 2535
 |||||
Sbjct: 671 tgagacaatgg 661

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4477 taaagcctttg 4487
 |||||
Sbjct: 310 taaagcctttg 300

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2521 ctcttgagaca 2531
 |||||
Sbjct: 229 ctcttgagaca 219

Lambda	K	H
1.37	0.711	1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 38
Number of Sequences: 0
Number of extensions: 38
Number of successful extensions: 38
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 29
length of query: 5253
length of database: 4392
effective HSP length: 12
effective length of query: 5241
effective length of database: 4380
effective search space: 22955580
effective search space used: 22955580
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 11 (22.3 bits)

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) 

About Entrez

Show difference in format

Entrez

Gi	Version	Update Date
4539617	1	Mar 30 1999 12:03
4559409	2	Apr 5 1999 1:29

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Query= gi|4539617|gb|U95825.1|HSU95825 Human androgen-induced prost proliferative shutoff associated protein (AS3) mRNA, complete cds (4392 letters)

Help/FAQ

<gi|4559409|gb|U95825.2|HSU95825 Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds
Length = 5253

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

Score = 7547 bits (3807), Expect = 0.0
Identities = 3953/4017 (98%)
Strand = Plus / Plus

Check sequence revision history

Query: 1 ggatacaaaagagcccacaaattcaataggtatTTTTATTtacttgagaacattgct
Sbjct: 419 ggatacaaaagagcccacagttcaataggtatTTTTATTtcttgagaacattgct

How to create WWW links to Entrez

Query: 61 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcaccac
Sbjct: 479 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcaccac

LinkOut

Cubby

Query: 121 cagaaccttattttcagttataaacaatggccacaatcagaaagtccatatgca
Sbjct: 539 cagaaccttattttcagttataaacaatggccacaatcagaaagtccatatgca

Related resources

BLAST

Query: 181 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt
Sbjct: 599 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt

Reference sequence project

LocusLink

Query: 241 ggtttttagtaaatctggtacctgctcataagaatttaaacagcaagcatatgat
Sbjct: 659 ggtttttagtaaatctggtacctgctcataagaatttaaacagcaagcatatgat

Clusters of orthologous groups

Protein reviews on the web

Query: 301 aaaggctttactgaagaggacagctcaagctattgagccatatattaccacnnr
Sbjct: 719 aaaggctttactgaagaggacagctcaagctattgagccatatattaccaattt

Query: 361 tcaggttctgatgcttgggaaaacatctatcagcgatttgtcagagcatgtctt

```
|||||
Sbjct: 779 tcagggttctgatgcttgggaaaacatctatcagcgatttgtcagagcatgtctct

Query: 421 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca
|||||
Sbjct: 839 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca

Query: 481 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact
|||||
Sbjct: 899 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact

Query: 541 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca
|||||
Sbjct: 959 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca

Query: 601 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt
|||||
Sbjct: 1019 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt

Query: 661 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa
|||||
Sbjct: 1079 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa

Query: 721 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac
|||||
Sbjct: 1139 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac

Query: 781 taaaaaggatattcttctggtcaatgatcacttacttaattttgtgagagagag
|||||
Sbjct: 1199 taaaaaggatattcttctggtcaatgatcacttacttaattttgtgggagagag

Query: 841 agacaaacgatggagagtagcgaagaagccatgatgggacttgcccaaatttat
|||||
Sbjct: 1259 agacaaacgatggagagtagcgaagaagccatgatgggacttgcccaaatttat

Query: 901 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat
|||||
Sbjct: 1319 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat

Query: 961 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa
|||||
Sbjct: 1379 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa

Query: 1021 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg
|||||
Sbjct: 1439 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg

Query: 1081 ttacttgatgccacactggatttaaagtctgtgaaagcattgaatgaaatgtg
```

Sbjct: 1499 |ttacttg|tatgcc|actgg|atttaa|atgctgt|gaaagc|attgaa|tgaaat|gtgga|
Query: 1141 |tcaaaat|ctgctcc|gacatca|agtaaag|gatttg|cttgact|tgatta|agcaacc|
Sbjct: 1559 |tcaaaat|ctgctcc|gacatca|agtaaag|gatttg|cttgact|tgatta|agcaacc|
Query: 1201 |agatgcc|agtgtca|aggccat|atTTTT|caaaagt|gatgggt|attaca|agaaattt|
Sbjct: 1619 |agatgcc|agtgtca|aggccat|atTTTT|caaaagt|gatgggt|attaca|agaaattt|
Query: 1261 |tcttggt|aaggctc|aggattt|catgaa|gaaattc|acacagg|tgtaga|agatgat|
Sbjct: 1679 |tcttggt|aaggctc|aggattt|catgaa|gaaattc|acacagg|tgtaga|agatgat|
Query: 1321 |aataaga|aagcagt|tagaagt|acttg|ttagt|ccaacat|gctcct|gcaagc|aggct|
Sbjct: 1739 |aataaga|aagcagt|tagaagt|acttg|ttagt|ccaacat|gctcct|gcaagc|aggct|
Query: 1381 |ttgtgtg|cgtgaa|ataacta|agaagt|tggtgg|gcaacccc|aaacag|cctacaa|atcct|
Sbjct: 1799 |ttgtgtg|cgtgaa|ataacta|agaagt|tggtgg|gcaacccc|aaacag|cctacaa|atcct|
Query: 1441 |ggaaatg|atcaagt|ttctctt|ggagagg|atagcac|ctgtgcac|atagata|accga|
Sbjct: 1859 |ggaaatg|atcaagt|ttctctt|ggagagg|atagcac|ctgtgcac|atagata|accga|
Query: 1501 |cagtgtc|tctatta|taacaag|tgaacaa|atcaata|gatggaac|agcagat|gatgaa|
Sbjct: 1919 |cagtgtc|tctatta|taacaag|tgaacaa|atcaata|gatggaac|agcagat|gatgaa|
Query: 1561 |gggtgtt|ccaactg|atcaagc|catcagag|caggtctt|gaactg|cttaagg|tactc|
Sbjct: 1979 |gggtgtt|ccaactg|atcaagc|catcagag|caggtctt|gaactg|cttaagg|tactc|
Query: 1621 |tacacat|cccattc|tctcattt|ctgctgaa|acatttg|aatcatt|actggct|tgt|
Sbjct: 2039 |tacacat|cccattc|tctcattt|ctgctgaa|acatttg|aatcatt|actggct|tgt|
Query: 1681 |aatggat|gatgaaa|aagtagc|agaagct|gcactaca|aatTTTT|caaaaac|acagg|
Sbjct: 2099 |aatggat|gatgaaa|aagtagc|agaagct|gcactaca|aatTTTT|caaaaac|acagg|
Query: 1741 |aattgaa|gaggatt|tttccac|acatcagat|cagcctt|gcttctc|gttttac|atcac|
Sbjct: 2159 |aattgaa|gaggatt|tttccac|acatcagat|cagcctt|gcttctc|gttttac|atcac|
Query: 1801 |taaaaaa|aggannn|nnnnngt|caagcca|aatatgc|cattcatt|gtatccat|gcatc|

Sbjct: 2219 taaaaaaggaccccccggtcaagccaaatatgccattcattgtatccatgcgata
Query: 1861 tagtaaagagaccagtttgacagatatattgagcctctgcataagagcctagat
Sbjct: 2279 tagtaaagaggccagtttgacagatatattgagcctctgcataagagcctagat
Query: 1921 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Sbjct: 2339 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Query: 1981 tgatcaatttgctgctccttggaatcttgggtagctactttcattgtgaaagat
Sbjct: 2399 tgatcaatttgctgctccttggaatcttgggtagctactttcattgtgaaagat
Query: 2041 catgaatgatcggttccagggaaaaagacaactaaactttgggttccagatga
Sbjct: 2459 catgaatgatcggttccagggaaaaagacaactaaactttgggttccagatga
Query: 2101 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Sbjct: 2519 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Query: 2161 aatgaaaaataatcacagtaaatcaggaacttctaccttaagattgctaacaaca
Sbjct: 2579 aatgaaaaataatcacagtaaatcaggaacttctaccttaagattgctaacaaca
Query: 2221 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Sbjct: 2639 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Query: 2281 gagacttgctgctgggagtgtatttgtgaagctggcacaagaaccctgttaccat
Sbjct: 2699 gagacttgctgctgggagtgtatttgtgaagctggcacaagaaccctgttaccat
Query: 2341 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Sbjct: 2759 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Query: 2401 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Sbjct: 2819 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Query: 2461 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Sbjct: 2879 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Query: 2521 taggcaatgtttggtgaaaaatataaatgtaaggcgaggatctgaagcagcat

Sbjct: 2939 taggcaatgtttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat
Query: 2581 tgtagtgaaaaattattgtctcttctaccagagtatgtagtccatataacaatt
Sbjct: 2999 tgtagtgaaaaattattgtctcttctaccagagtatgtagtccatataacaatt
Query: 2641 ttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Sbjct: 3059 ttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Query: 2701 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Sbjct: 3119 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Query: 2761 ttttatcagaaagatggtagaaaatattaacaaacaaaagatgcccaaggacc
Sbjct: 3179 ttttatcagaaagatggtagaaaatattaagcaaaacaaaagatgcccaaggacc
Query: 2821 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Sbjct: 3239 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Query: 2881 aaagagtactacatacagtttggaatctcctaagacccggtactaccagctcgt
Sbjct: 3299 aaagagtactacatacagtttggaatctcctaagacccggtactaccagctcgt
Query: 2941 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctgaaatc
Sbjct: 3359 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctggaatc
Query: 3001 atttttcactcctggaaaacctaaaacaaccaatgttctaggagctgttaacaac
Sbjct: 3419 atttttcactcctggaaaacctaaaacaaccaatgttctaggagctgttaacaac
Query: 3061 ttcatcagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaagc
Sbjct: 3479 ttcatcagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc
Query: 3121 aagcagcagctcaaatacaagctctcctggaagaataaagggaggcttgatagt
Sbjct: 3539 aagcagcagctcaaatacaagctctcctggaagaataaagggaggcttgatagt
Query: 3181 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggnnr
Sbjct: 3599 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa
Query: 3241 tgacaagagagacgactctgatcttgtaaggctctgaattggagaagcctagaggc

Sbjct: 3659 |tgacaagagagacgactctgatcttgtaaggtctgaattggagaagcctagagg|

Query: 3301 |nnnnncgcccgtcacagaacaggaggagaaattaggtatggatgacttgactaa|

Sbjct: 3719 |aaaaacgcccgtcacagaacgggaggagaaattaggtatggatgacttgactaa|

Query: 3361 |acaggaacagaaacctaagggcagtcagcgaagtcggaaaagaggccatacggct|

Sbjct: 3779 |acaggaacagagacctaagggcagtcagcgaagtcggaaaagaggccatacggct|

Query: 3421 |atctgatgaacagcagtggcctgaggaaaagaggctcaaagaagatatattaga|

Sbjct: 3839 |atctgatgaacagcagtggcctgaggaaaagaggctcaaagaagatatattaga|

Query: 3481 |agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccacccaaaacct|

Sbjct: 3899 |agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccacccaaaacct|

Query: 3541 |tggaggtaacacaaaagaagagccaacaatgaaaacttctaaaaaaggaagcnn|

Sbjct: 3959 |tggaggtaacacaaaagaagagccaacaatgaaaacttctaaaaaaggaagcaa|

Query: 3601 |ntctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat|

Sbjct: 4019 |atctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat|

Query: 3661 |acagaagtccaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagc|

Sbjct: 4079 |acagaagtccaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagc|

Query: 3721 |tcctgaatctagtgcattgaatccacacagtcacacaccagaaaggacgagg|

Sbjct: 4139 |tcctgaatctagtgcattgaatccacacagtcacacaccagaaaggacgagg|

Query: 3781 |atcaaaaacgccatcaccatcacaaccnnnnnnntgtgtaagttgtaaatatt|

Sbjct: 4199 |atcaaaaacgccatcaccatcacaaccnaaaatgtgtaagttgtaaatatt|

Query: 3841 |tcaaaccaatttcaaattattttgcaaaagttcctaaatttgtaaacatacatat|

Sbjct: 4259 |tcaaaccaatttcaaattattttgcaaaagttcctaaatttgtaaacatacatat|

Query: 3901 |tatttaaattccatatatttagccccattacactaggtacggcggcgaagtgct|

Sbjct: 4319 |tatttaaattccatatatttagccccattacactaggtacggcggcgaagtgct|

Query: 3961 |gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaa|

|||||
Sbjct: 4379 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaaa

Score = 396 bits (200), Expect = e-113

Identities = 200/200 (100%)

Strand = Plus / Plus

Query: 4040 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

|||||
Sbjct: 4458 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

Query: 4100 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

|||||
Sbjct: 4518 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

Query: 4160 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga

|||||
Sbjct: 4578 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga

Query: 4220 agaagaaacttgtaaataatc 4239

|||||
Sbjct: 4638 agaagaaacttgtaaataatc 4657

Score = 274 bits (138), Expect = 7e-76

Identities = 138/138 (100%)

Strand = Plus / Plus

Query: 4255 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga

|||||
Sbjct: 4673 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga

Query: 4315 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta

|||||
Sbjct: 4733 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta

Query: 4375 taatctgtcagtgtttgt 4392

|||||
Sbjct: 4793 taatctgtcagtgtttgt 4810

Score = 26.3 bits (13), Expect = 0.28

Identities = 13/13 (100%)

Strand = Plus / Minus

Query: 1525 caaatcaatagat 1537

|||||
Sbjct: 4761 caaatcaatagat 4749

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 4331 atctattgatttg 4343
 |||||
Sbjct: 1955 atctattgatttg 1943

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 3633 aagaagaaaga 3643
 |||||
Sbjct: 5118 aagaagaaaga 5128

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1524 acaaatcaata 1534
 |||||
Sbjct: 5079 acaaatcaata 5069

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 300 caaaggcttta 310
 |||||
Sbjct: 4487 caaaggcttta 4477

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1966 tgctctccttg 1976
 |||||
Sbjct: 4121 tgctctccttg 4111

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)

Strand = Plus / Minus

Query: 1889 tttgagcctct 1899
 |||||||
Sbjct: 3878 tttgagcctct 3868

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 661 ccattgtctca 671
 |||||||
Sbjct: 2535 ccattgtctca 2525

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 219 tgtctcaggag 229
 |||||||
Sbjct: 2531 tgtctcaggag 2521

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3693 caaggagagca 3703
 |||||||
Sbjct: 2394 caaggagagca 2384

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3450 agaggctcaaa 3460
 |||||||
Sbjct: 2317 agaggctcaaa 2307

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1730 acaggaagcaa 1740
 |||||||

Sbjct: 2203 acaggaagcaa 2193

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1775 ttgcttcctgt 1785

|||||||

Sbjct: 2158 ttgcttcctgt 2148

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2107 tgagacaatgg 2117

|||||||

Sbjct: 1089 tgagacaatgg 1079

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4059 taaagcctttg 4069

|||||||

Sbjct: 728 taaagcctttg 718

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2103 ctcctgagaca 2113

|||||||

Sbjct: 647 ctcctgagaca 637

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 1620 ttacacatccc 1630

|||||||

Sbjct: 353 ttacacatccc 363

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 39
Number of Sequences: 0
Number of extensions: 39
Number of successful extensions: 39
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 29
length of query: 4392
length of database: 5253
effective HSP length: 12
effective length of query: 4380
effective length of database: 5241
effective search space: 22955580
effective search space used: 22955580
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 11 (22.3 bits)

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)